

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 08:47:22 ; Search time 0.001 Seconds
(without alignments)
167.310 Million cell updates/sec

Title: us-09-762-258-2

Perfect score: 2614
Sequence: 1 MARGRRRAGAGAAAVFDL.....PIRPPSGTKKRGRRPGR 495

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 338 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : us-09-153-939-2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1692	64.7	338	1 us-09-153-939-2

ALIGNMENTS

RESULT 1
us-09-153-939-2

Query Match 64.7%; Score 1692; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	181	EDTACFYLAETTLALGHLISOGIIYRDIKPENIMLSSOGHKLTDPGICKESIHEGAVTH	240
DB	24	EDTACFYLAETTLALGHLISOGIIYRDIKPENIMLSSOGHKLTDPGICKESIHEGAVTH	83
QY	241	TFGGTIEYMADEIIVSGHNRADVMSIGALMYDMLTGSPPETAENRKKTMDIIRGKLA	300
DB	84	TFGGTIEYMADEIIVSGHNRADVMSIGALMYDMLTGSPPETAENRKKTMDIIRGKLA	143
QY	301	LPPIYLPDARLUYKELKXNBSORIGGGPGADVORHPRFRHNMMDLLAMRVDPFRP	360
DB	144	LPPIYLPDARLUYKELKXNBSORIGGGPGADVORHPRFRHNMMDLLAMRVDPFRP	203
QY	361	CTQSEEDVSGPDTFTQTPVDSPDPTALSESANQAFGLTYVAPSVLDSIKGFSFOPK	420
DB	204	CTQSEEDVSGPDTFTQTPVDSPDPTALSESANQAFGLTYVAPSVLDSIKGFSFOPK	263
QY	421	LSPPRLNLSRVVSVPLKSPFBGFRPSBSPBETELPLPPLPPEPSTTAPLPFRP	480
DB	264	LSPPRLNLSRVVSVPLKSPFBGFRPSBSPBETELPLPPLPPEPSTTAPLPFRP	323

QY 481 SGTKKKRGRRPGR 495
DB 324 SGTKKKRGRRPGR 338

Search completed: March 18, 2004, 08:47:22
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	181	EDTACEFYAARTLALGHLSOGITRYDLKPEINMISOGHITKLTDFGLCKESIHEGAYTH	240
DB	24	EDTACFYAETLTLALGHLSOGITRYDLKPEINMISOGHITKLTDFGLCKESIHEGAYTH	83
QY	241	TECGTIEYMAPEILVSGNRAVDWMSIGALMYDMLTGSPPETAENRKKTMDKIIRGKLA	300
DB	84	TECGTIEYMAPEILVSGNRAVDWMSIGALMYDMLTGSPPETAENRKKTMDKIIRGKLA	143
QY	301	LPPYLTPDARDLYKKFLKRNPSQRIIGGPGDADVQRHPPFRHNMWDDLAMRVDPFRP	360
DB	144	LPPYLTPDARDLYKKFLKRNPSQRIIGGPGDADVQRHPPFRHNMWDDLAMRVDPFRP	203
QY	361	CLOSEEDYSQDFTRFROTTPVDSPPDTALSESANQAFGLTYVAPSVLDSIKGFSFOPK	420
DB	204	CLOSEEDYSQDFTRFROTTPVDSPPDTALSESANQAFGLTYVAPSVLDSIKGFSFOPK	263
QY	421	LSPPRLNLSRPVPSPLKSPFEGFRSPSLPEPTLPLPPLPPPGSTTAPLPIRPP	480
DB	264	LSPPRLNLSRPVPSPLKSPFEGFRSPSLPEPTLPLPPLPPPGSTTAPLPIRPP	323

QY 481 SGTKKSKRGGRGR 495
DB 324 SGTKKSKRGGRGR 338

Search completed: March 18, 2004, 08:47:22
Job time : 0.001 secs

QY	89	CGAGGGGCCCCGGGGGCGGAGCGCGCAATGCGCGCGCTTTGATTGATTGGAGACG	148
Db	1	CGAGGGGCCCCGGGCGGCGG-----CGCAATGCGCGCGCTTTGATTGATTGGAGACG	56
QY	149	GAGGAAAGCGAGCGAGGCGTAGGCGGAGCCCAAGCTCAAGCCCGCGAGCGATGTCCTTT	208
Db	57	GAGGAAAGCGAGCGAGGCGTAGGCGGAGCCCAAGCTCAAGCCCGCGG-----	101
QY	209	GCCGAGTTGAGGCGAGCTGGGCTAGAGCGCTGGGCAACTATGAAGAAGTGAGAGTACT	268
Db	102	-----GCTGTGGGACATATGAAGAAGTGAGAGTACT	135
QY	269	GAGACGAGGTGAACGTTGSCCCAGAGCGCATGCGGACCCCACTGCTTGAAGCTGTGCT	328
Db	136	GAGACGAGGTGAACGTTGSCCCAGAGCGCATGCGGACCCCACTGCTTGAAGCTGTGCT	195
QY	329	GTCGTGGGCGAAGGGGGCGTATNGGCAAGGTGTCCAGGTGCGAAGAAGTGCACAGCCAC	388
Db	196	GTCGTGGGCGAAGGGGGCGTATNGCAAGGTGTCCAGGTGCGAAGAAGTGCACAGCCAC	255

QY	389	TTGGGCAAAAATATATGCAATGAAAGTCTTATGGAAGGCAAAAATTGTGGCAATGCGAAG	448
Db	236	TTGGGCAAAAATATATGCAATGAAAGTCTTATGGAAGGCAAAAATTGTGGCAATGCGAAG	315
QY	449	GACACGACACACACACG99GCTAGCGGAACTTTTATAGTACGTAAAGCACCCCTTTATT	508
Db	316	GACACGACACACACACG99GCTAGCGGAACTTTTATAGTACGTAAAGCACCCCTTTATT	375
QY	509	GTTGAATCTGGGCTTATGCTTCCAGCTGTGTGTGAAATCTTACCTCATCTGTGATGTCTTC	568
Db	376	GTTGAATCTGGGCTTATGCTTCCAGCTGTGTGTGAAATCTTACCTCATCTGTGATGTCTTC	435
QY	569	AGTGTGTGTGAGCTCTTCAACGATCTGTGACGAGG9GCACTTCTGTGAAATATGCGCC	628
Db	436	AGTGTGTGTGAGCTCTTCTCG-----GGAAATATATGCGCC	469
QY	629	TGCTTTACTCTGTGTGATACGCTGTGCCCTTGGGCACTTCCATCTTCCAGGGCACTATC	688
Db	470	TGCTTTACTCTGTGTGATACGCTGTGCCCTTGGGCACTTCCATCTTCCAGGGCACTATC	529
QY	689	TACCGG9AAGCTTCAAGCCCGAGAAACATCATCTGTAGACACAGGGGCACTCAATCAATGACC	748
Db	530	TACCGG9AAGCTTCAAGCCCGAGAAACATCATCTGTAGACACAGGGGCACTCAATCAATGACC	589
QY	749	GACTTTGACCTCTGCAGAGATCTTATCATAGAGG9GCGCCCTACTCACTCTTCTGCGGC	808
Db	590	GACTTTGACCTCTGCAGAGATCAATCAATGAGG9GCGCCCTACTCACTCTTCTGCGGC	649
QY	809	ACCATTTGATATCATAGGCGCCCTGATCTGTGTGTGCGAGTGTGCACAAACCG99GCTGTGAC	868
Db	650	ACCATTTGATATCATAGGCGCCCTGATCTGTGTGTGCGAGTGTGCACAAACCG99GCTGTGAC	709
QY	869	TGTGTGAGGCTGTGG9GCGCTGTATGTATGACATGCTCATGTGATGCGCGCCCTTTATACGCA	928
Db	710	TGTGTGAGGCTGTGG9GCGCTGTATGTATGACATGCTCATGTGATGCGCGCCCTTTATACGCA	769
QY	929	GAGAACCG9AAGAAAACATGATTAATCATATAGGGGCAAGCTG9CACTGTCCCCCTTAC	988
Db	770	GAGAACCG9AAGAAAACATGATTAATCATATAGGGGCAAGCTG9CACTGTCCCCCTTAC	829
QY	989	CTCACCCGATGTGCGCG9GACCTTGTCAAAAATTTCGAAACG9AATCCAGCCACAGCG	1048
Db	830	CTCACCCGATGTGCGCG9GACCTTGTCAAAAATTTCGAAACG9AATCCAGCCACAGCG	889
QY	1049	ATTGTGGGCTGTGGCCCAAGGG9ATGTCTGTGATGTGTGAGACATCTCTTTTTCG9GCAATG	1108
Db	890	ATTGTGGGCTGTGGCCCAAGGG9ATGTCTGTGATGTGTGAGACATCTCTTTTTCG9GCAATG	949
QY	1109	AATTTGG9AAGCACTTCTGTG9GCTGTGTGTG9AAGCCCTTTCAG9GCTGTGTGAGTCA	1168
Db	950	AATTTGG9AAGCACTTCTGTG9GCTGTGTGTG9AAGCCCTTTCAG9GCTGTGTGAGTCA	1008
QY	1169	GAGGAG9AAGCTGTAGCCAGTTTATATCCCGCTTCAACG9GACAGCGCGGTGTGACATGCTCT	1228
Db	1010	GAGGAG9AAGCTGTAGCCAGTTTATATCCCGCTTCAACG9GACAGCGCGGTGTGACATGCTCT	1068
QY	1229	GATGTACAG9GCTGTACAGAGT	1288
Db	1070	GATGTACAG9GCTGTACAGAGT	1128
QY	1289	CCGTGTGTCTGTGACAGACATCAGAGAG9GCTTCTCTTTCAGGCGCAGAGCTGTG9CTCAACC	1348
Db	1130	CCGTGTGTCTGTGACAGACATCAGAGAG9GCTTCTCTTTCAGGCGCAGAGCTGTG9CTCAACC	1188
QY	1349	AGGAGGCTTCAACATGACCCCGGGGTCCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1408
Db	1190	AGGAGGCTTCAACATGACCCCGGGGTCCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1248
QY	1409	GAGTTTGTG9GCTTCAAGGCTTGT	1468
Db	1250	GAGTTTGTG9GCTTCAAGGCTTGT	1308
QY	1469	CCACCGGCGGCTTGTGACACAGGCGCTTCTTCCCATTCGTCCTCCCTTCAG9GACATGAC	1528

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Db      1310  CCAACGCGCGCCCTCGACCCGCCCTCTCCCATCCGTCCGCCCTCAGGGACCAAG 1369
QY      1529  AAGTCCAAGAGGGGCCGTTGAGGGGCTAGGAGCGGGTGGGGGTGAGGGTAG 1588
Db      1370  AAGTCCAAGAGGGGCGTGGGCGTCCAGGGCGCTAGGAGCGGGTGGGGGTGAGGGTAG 1429
QY      1589  CCTTGAAGCCTGTCTGCGGCTGTGAGAGCAGAGAACCTGGGCGAGTCCAGAGAC 1648
Db      1430  CCTTGAAGCCTGTCTGCGGCTGTGAGAGCAGAGAACCTGGGCGAGTCCAGAGAC 1489
QY      1649  CTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGGTGAAGGTGTGTCTGTGGGGCA 1708
Db      1490  CTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGGTGAAGGTGTGTCTGTGGGGCA 1549
QY      1709  GCTGTGCCCCGTAATCATGGGCAAGGAGGCGCGCGCAACCCCGGCTCAACTGCTC 1768
Db      1550  GCTGTGCCCCGTAATCATGGGCAAGGAGGCGCGCGCAACCCCGGCTCAACTGCTC 1609
QY      1769  CCGTGAAGATTAAAGGCTGAATCATGAAAAAAAA 1806
Db      1610  CCGTGAAGATTAAAGGCTGAATCATGAAAAAAAA 1647
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Search completed: March 18, 2004, 08:51:23
Job time : 2 secs